

## SEQUENCE LISTING

<110> Yasuhiko MUNAKATA et al.

<120> Novel human parvovirus B19 receptor and uses thereof

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<211> 732

<212> PRT

10 <213> Homo sapiens

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35 40 45

Glu Asn Lys Asp Glu Ile Ala Leu Val Leu Phe Gly Thr Asp Gly Thr

50 55 60

20 Asp Asn Pro Leu Ser Gly Gly Asp Gln Tyr Gln Asn Ile Thr Val His

65 70 75 80

Arg His Leu Met Leu Pro Asp Phe Asp Leu Leu Glu Asp Ile Glu Ser

85 90 95

Lys Ile Gln Pro Gly Ser Gln Gln Ala Asp Phe Leu Asp Ala Leu Ile

25 100 105 110

Val Ser Met Asp Val Ile Gln His Glu Thr Ile Gly Lys Lys Phe Glu

115 120 125

Lys Arg His Ile Glu Ile Phe Thr Asp Leu Ser Ser Arg Phe Ser Lys  
 130 135 140  
 Ser Gln Leu Asp Ile Ile Ile His Ser Leu Lys Lys Cys Asp Ile Ser  
 145 150 155 160  
 5 Leu Gln Phe Phe Leu Pro Phe Ser Leu Gly Lys Glu Asp Gly Ser Gly  
 165 170 175  
 Asp Arg Gly Asp Gly Pro Phe Arg Leu Gly Gly His Gly Pro Ser Phe  
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 Pro Leu Lys Gly Ile Thr Glu Gln Gln Lys Glu Gly Leu Glu Ile Val  
 10 195 200 205  
 Lys Met Val Met Ile Ser Leu Glu Gly Glu Asp Gly Leu Asp Glu Ile  
 210 215 220  
 Tyr Ser Phe Ser Glu Ser Leu Arg Lys Leu Cys Val Phe Lys Lys Ile  
 225 230 235 240  
 15 Glu Arg His Ser Ile His Trp Pro Cys Arg Leu Thr Ile Gly Ser Asn  
 245 250 255  
 Leu Ser Ile Arg Ile Ala Ala Tyr Lys Ser Ile Leu Gln Glu Arg Val  
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 Lys Lys Thr Trp Thr Val Val Asp Ala Lys Thr Leu Lys Lys Glu Asp  
 20 275 280 285  
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 Val Leu Lys Glu Asp Ile Ile Gln Gly Phe Arg Tyr Gly Ser Asp Ile  
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 25 Val Pro Phe Ser Lys Val Asp Glu Glu Gln Met Lys Tyr Lys Ser Glu  
 325 330 335  
 Gly Lys Cys Phe Ser Val Leu Gly Phe Cys Lys Ser Ser Gln Val Gln

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	355	360	365
	Asp Asp Glu Ala Ala Ala Val Ala Leu Ser Ser Leu Ile His Ala Leu		
5	370	375	380
	Asp Asp Leu Asp Met Val Ala Ile Val Arg Tyr Ala Tyr Asp Lys Arg		
	385	390	395
	Ala Asn Pro Gln Val Gly Val Ala Phe Pro His Ile Lys His Asn Tyr		
	405	410	415
10	Glu Cys Leu Val Tyr Val Gln Leu Pro Phe Met Glu Asp Leu Arg Gln		
	420	425	430
	Tyr Met Phe Ser Ser Leu Lys Asn Ser Lys Lys Tyr Ala Pro Thr Glu		
	435	440	445
	Ala Gln Leu Asn Ala Val Asp Ala Leu Ile Asp Ser Met Ser Leu Ala		
15	450	455	460
	Lys Lys Asp Glu Lys Thr Asp Thr Leu Glu Asp Leu Phe Pro Thr Thr		
	465	470	475
	Lys Ile Pro Asn Pro Arg Phe Gln Arg Leu Phe Gln Cys Leu Leu His		
	485	490	495
20	Arg Ala Leu His Pro Arg Glu Pro Leu Pro Pro Ile Gln Gln His Ile		
	500	505	510
	Trp Asn Met Leu Asn Pro Pro Ala Glu Val Thr Thr Lys Ser Gln Ile		
	515	520	525
	Pro Leu Ser Lys Ile Lys Thr Leu Phe Pro Leu Ile Glu Ala Lys Lys		
25	530	535	540
	Lys Asp Gln Val Thr Ala Gln Glu Ile Phe Gln Asp Asn His Glu Asp		
	545	550	555
			560

	Gly	Pro	Thr	Ala	Lys	Lys	Leu	Lys	Thr	Glu	Gln	Gly	Gly	Ala	His	Phe
					565					570					575	
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					580					585					590	
5	Asn	Pro	Ala	Glu	Asn	Phe	Arg	Val	Leu	Val	Lys	Gln	Lys	Lys	Ala	Ser
					595					600					605	
	Phe	Glu	Glu	Ala	Ser	Asn	Gln	Leu	Ile	Asn	His	Ile	Glu	Gln	Phe	Leu
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10	625					630						635				640
	Ala	Phe	Arg	Glu	Glu	Ala	Ile	Lys	Phe	Ser	Glu	Glu	Gln	Arg	Phe	Asn
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	Asn	Phe	Leu	Lys	Ala	Leu	Gln	Glu	Lys	Val	Glu	Ile	Lys	Gln	Leu	Asn
					660					665					670	
15	His	Phe	Trp	Glu	Ile	Val	Val	Gln	Asp	Gly	Ile	Thr	Leu	Ile	Thr	Lys
					675					680					685	
	Glu	Glu	Ala	Ser	Gly	Ser	Ser	Val	Thr	Ala	Glu	Glu	Ala	Lys	Lys	Phe
					690					695					700	
	Leu	Ala	Pro	Lys	Asp	Lys	Pro	Ser	Gly	Asp	Thr	Ala	Ala	Val	Phe	Glu
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<212> DNA

<213> Homo sapiens

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Met Val Arg Ser Gly Asn Lys Ala Ala

1

5

5

gtt gtg ctg tgt atg gac gtg ggc ttt acc atg agt aac tcc att cct 102

Val Val Leu Cys Met Asp Val Gly Phe Thr Met Ser Asn Ser Ile Pro

10

15

20

25

10

ggc ata gaa tcc cca ttt gaa caa gca aag aag gtg ata acc atg ttt 150

Gly Ile Glu Ser Pro Phe Glu Gln Ala Lys Lys Val Ile Thr Met Phe

30

35

40

gta cag cga cag gtg ttt gct gag aac aag gat gag att gct tta gtc 198

15

Val Gln Arg Gln Val Phe Ala Glu Asn Lys Asp Glu Ile Ala Leu Val

45

50

55

ctg ttt ggt aca gat ggc act gac aat ccc ctt tct ggt ggg gat cag 246

Leu Phe Gly Thr Asp Gly Thr Asp Asn Pro Leu Ser Gly Gly Asp Gln

20

60

65

70

tat cag aac atc aca gtg cac aga cat ctg atg cta cca gat ttt gat 294

Tyr Gln Asn Ile Thr Val His Arg His Leu Met Leu Pro Asp Phe Asp

75

80

85

25

ttg ctg gag gac att gaa agc aaa atc caa cca ggt tct caa cag gct 342

Leu Leu Glu Asp Ile Glu Ser Lys Ile Gln Pro Gly Ser Gln Gln Ala

	90	95	100	105	
	gac ttc ctg gat gca cta atc gtg agc atg gat gtg att caa cat gaa				390
	Asp Phe Leu Asp Ala Leu Ile Val Ser Met Asp Val Ile Gln His Glu				
5		110	115	120	
	aca ata gga aag aag ttt gag aag agg cat att gaa ata ttc act gac				438
	Thr Ile Gly Lys Lys Phe Glu Lys Arg His Ile Glu Ile Phe Thr Asp				
		125	130	135	
10	ctc agc agc cga ttc agc aaa agt cag ctg gat att ata att cat agc				486
	Leu Ser Ser Arg Phe Ser Lys Ser Gln Leu Asp Ile Ile Ile His Ser				
		140	145	150	
15	ttg aag aaa tgt gac atc tcc ctg caa ttc ttc ttg cct ttc tca ctt				534
	Leu Lys Lys Cys Asp Ile Ser Leu Gln Phe Phe Leu Pro Phe Ser Leu				
		155	160	165	
	ggc aag gaa gat gga agt ggg gac aga gga gat ggc ccc ttt cgc tta				582
20	Gly Lys Glu Asp Gly Ser Gly Asp Arg Gly Asp Gly Pro Phe Arg Leu				
	170	175	180	185	
	ggt ggc cat ggg cct tcc ttt cca cta aaa gga att acc gaa cag caa				630
	Gly Gly His Gly Pro Ser Phe Pro Leu Lys Gly Ile Thr Glu Gln Gln				
25		190	195	200	
	aaa gaa ggt ctt gag ata gtg aaa atg gtg atg ata tct tta gaa ggt				678

	Lys Glu Gly Leu Glu Ile Val Lys Met Val Met Ile Ser Leu Glu Gly	
	205 210 215	
5	gaa gat ggg ttg gat gaa att tat tca ttc agt gag agt ctg aga aaa Glu Asp Gly Leu Asp Glu Ile Tyr Ser Phe Ser Glu Ser Leu Arg Lys	726
	220 225 230	
10	ctg tgc gtc ttc aag aaa att gag agg cat tcc att cac tgg ccc tgc Leu Cys Val Phe Lys Lys Ile Glu Arg His Ser Ile His Trp Pro Cys	774
	235 240 245	
15	cga ctg acc att ggc tcc aat ttg tct ata agg att gca gcc tat aaa Arg Leu Thr Ile Gly Ser Asn Leu Ser Ile Arg Ile Ala Ala Tyr Lys	822
	250 255 260 265	
20	tcg att cta cag gag aga gtt aaa aag act tgg aca gtt gtg gat gca Ser Ile Leu Gln Glu Arg Val Lys Lys Thr Trp Thr Val Val Asp Ala	870
	270 275 280	
25	aaa acc cta aaa aaa gaa gat ata caa aaa gaa aca gtt tat tgc tta Lys Thr Leu Lys Lys Glu Asp Ile Gln Lys Glu Thr Val Tyr Cys Leu	918
	285 290 295	
30	aat gat gat gat gaa act gaa gtt tta aaa gag gat att att caa ggg Asn Asp Asp Asp Glu Thr Glu Val Leu Lys Glu Asp Ile Ile Gln Gly	966
	300 305 310	

	ttc cgc tat gga agt gat ata gtt cct ttc tct aaa gtg gat gag gaa	1014
	Phe Arg Tyr Gly Ser Asp Ile Val Pro Phe Ser Lys Val Asp Glu Glu	
	315 320 325	
5	caa atg aaa tat aaa tcg gag ggg aag tgc ttc tct gtt ttg gga ttt	1062
	Gln Met Lys Tyr Lys Ser Glu Gly Lys Cys Phe Ser Val Leu Gly Phe	
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	tgt aaa tct tct cag gtt cag aga aga ttc ttc atg gga aat caa gtt	1110
10	Cys Lys Ser Ser Gln Val Gln Arg Arg Phe Phe Met Gly Asn Gln Val	
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	cta aag gtc ttt gca gca aga gat gat gag gca gct gca gtt gca ctt	1158
	Leu Lys Val Phe Ala Ala Arg Asp Asp Glu Ala Ala Ala Val Ala Leu	
15	365 370 375	
	tcc tcc ctg att cat gct ttg gat gac tta gac atg gtg gcc ata gtt	1206
	Ser Ser Leu Ile His Ala Leu Asp Asp Leu Asp Met Val Ala Ile Val	
	380 385 390	
20	cga tat gct tat gac aaa aga gct aat cct caa gtc ggc gtg gct ttt	1254
	Arg Tyr Ala Tyr Asp Lys Arg Ala Asn Pro Gln Val Gly Val Ala Phe	
	395 400 405	
25	cct cat atc aag cat aac tat gag tgt tta gtg tat gtg cag ctg cct	1302
	Pro His Ile Lys His Asn Tyr Glu Cys Leu Val Tyr Val Gln Leu Pro	
	410 415 420 425	

	ttc atg gaa gac ttg cgg caa tac atg ttt tca tcc ttg aaa aac agt	1350
	Phe Met Glu Asp Leu Arg Gln Tyr Met Phe Ser Ser Leu Lys Asn Ser	
	430 435 440	
5	aag aaa tat gct ccc acc gag gca cag ttg aat gct gtt gat gct ttg	1398
	Lys Lys Tyr Ala Pro Thr Glu Ala Gln Leu Asn Ala Val Asp Ala Leu	
	445 450 455	
10	att gac tcc atg agc ttg gca aag aaa gat gag aag aca gac acc ctt	1446
	Ile Asp Ser Met Ser Leu Ala Lys Lys Asp Glu Lys Thr Asp Thr Leu	
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	gaa gac ttg ttt cca acc acc aaa atc cca aat cct cga ttt cag aga	1494
15	Glu Asp Leu Phe Pro Thr Thr Lys Ile Pro Asn Pro Arg Phe Gln Arg	
	475 480 485	
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	Leu Phe Gln Cys Leu Leu His Arg Ala Leu His Pro Arg Glu Pro Leu	
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	ccc cca att cag cag cat att tgg aat atg ctg aat cct ccc gct gag	1590
	Pro Pro Ile Gln Gln His Ile Trp Asn Met Leu Asn Pro Pro Ala Glu	
	510 515 520	
25	gtg aca aca aaa agt cag att cct ctc tct aaa ata aag acc ctt ttt	1638
	Val Thr Thr Lys Ser Gln Ile Pro Leu Ser Lys Ile Lys Thr Leu Phe	

	525	530	535	
	cct ctg att gaa gcc aag aaa aag gat caa gtg act gct cag gaa att	1686		
	Pro Leu Ile Glu Ala Lys Lys Lys Asp Gln Val Thr Ala Gln Glu Ile			
5	540	545	550	
	ttc caa gac aac cat gaa gat gga cct aca gct aaa aaa tta aag act	1734		
	Phe Gln Asp Asn His Glu Asp Gly Pro Thr Ala Lys Lys Leu Lys Thr			
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10				
	gag caa ggg gga gcc cac ttc agc gtc tcc agt ctg gct gaa ggc agt	1782		
	Glu Gln Gly Gly Ala His Phe Ser Val Ser Ser Leu Ala Glu Gly Ser			
	570	575	580	585
15	gtc acc tct gtt gga agt gtg aat cct gct gaa aac ttc cgt gtt cta	1830		
	Val Thr Ser Val Gly Ser Val Asn Pro Ala Glu Asn Phe Arg Val Leu			
	590	595	600	
	gtg aaa cag aag aag gcc agc ttt gag gaa gcg agt aac cag ctc ata	1878		
20	Val Lys Gln Lys Lys Ala Ser Phe Glu Glu Ala Ser Asn Gln Leu Ile			
	605	610	615	
	aat cac atc gaa cag ttt ttg gat act aat gaa aca ccg tat ttt atg	1926		
	Asn His Ile Glu Gln Phe Leu Asp Thr Asn Glu Thr Pro Tyr Phe Met			
25	620	625	630	
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	Lys Ser Ile Asp Cys Ile Arg Ala Phe Arg Glu Glu Ala Ile Lys Phe	
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5	Ser Glu Glu Gln Arg Phe Asn Asn Phe Leu Lys Ala Leu Gln Glu Lys	
	650                                  655                                  660                                  665	
	gtg gaa att aaa caa tta aat cat ttc tgg gaa att gtt gtc cag gat	2070
	Val Glu Ile Lys Gln Leu Asn His Phe Trp Glu Ile Val Val Gln Asp	
10	670                                  675                                  680	
	gga att act ctg atc acc aaa gag gaa gcc tct gga agt tct gtc aca	2118
	Gly Ile Thr Leu Ile Thr Lys Glu Glu Ala Ser Gly Ser Ser Val Thr	
	685                                  690                                  695	
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	gct gag gaa gcc aaa aag ttt ctg gcc ccc aaa gac aaa cca agt gga	2166
	Ala Glu Glu Ala Lys Lys Phe Leu Ala Pro Lys Asp Lys Pro Ser Gly	
	700                                  705                                  710	
	gac aca gca gct gta ttt gaa gaa ggt ggt gat gtg gac gat tta ttg	2214
20	Asp Thr Ala Ala Val Phe Glu Glu Gly Gly Asp Val Asp Asp Leu Leu	
	715                                  720                                  725	
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25	Asp Met Ile	
	730	

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	tatatcactt cactgttctc tacttgcaag cctcaaagag agaaagtttc gttatattaa	3046
	aacacttagg taacttttctg gtctttccca tttctacctc agtcagcttt catctttgtg	3106
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